

SEQUENCE LISTING

<110> Ozelius, Laurie J.
Breakefield, Xandra O.

<120> TORSIN, TORSIN-RELATED GENES, AND
METHODS OF DETECTING NEURONAL DISEASES

<130> 0838.1001009

<150> 09/461,921
<151> 1999-12-15

<150> US 09/218,363
<151> 1998-12-22

<150> US 09/099,454
<151> 1998-06-18

<150> US 60/050,244
<151> 1997-06-19

<160> 90

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2597
<212> DNA
<213> Homo sapien

<220>
<221> CDS
<222> (568) ... (1563)

<221> misc_feature
<222> (1) ... (2597)
<223> n = A, T, C or G

<400> 1
ctgaaaatag ctncttatta ttattattat tattattatt atttgcggga gggagcacag 60
tcttgctctg tctcccaggc tggagntgca gtgggtgagat ctcggctcac tgcaatctcc 120
gcctcctggg ttcaagngca gttgctcatg tgtcagcctc cccagtagct agggctacag 180
gtgcctacca ccacaccggc taattttata ttttttagtag agacgtggtt tcaccatgtt 240
ggtcaggctg gtctcgaact cctgacactca ggtgatccgc ccncctcagc ctncccaaag 300
ggctgggatt acaggcagga gccaccatnc ctggaaaaaa taacgtccat aaacaaaaac 360
acgtggccaa caggcggag cagaaccgag tttccggaaag caaaacaggg ctttgcgttccg 420
aacaaagatg gcggccgccc gcgtcgggag gagggctgcc ctgaagaaag atggcctccg 480
cgagaggagg aanccggaag cgtgggtctg gcggctgcac cggttcgcgg tcggcgcgag 540
aacaaggcagg gtggcgcggg tccgggc atg aag ctg ggc cgg gcc gtg ggc 594

Met Lys Leu Gly Arg Ala Val Leu Gly
1 5

ctg ctg ctg ctg gcg ccg tcc gtg gtg cag gcg gtg gag ccc atc agc 642
Leu Leu Leu Leu Ala Pro Ser Val Val Gln Ala Val Glu Pro Ile Ser
10 15 20 25

ctg gga ctg gcc ctg gcc ggc gtc ctc acc ggc tac atc tac ccg cgt	690		
Leu Gly Leu Ala Leu Ala Gly Val Leu Thr Gly Tyr Ile Tyr Pro Arg			
30	35	40	
ctc tac tgc ctc ttc gcc gag tgc tgc ggg cag aag cgg agc ctt agc	738		
Leu Tyr Cys Leu Phe Ala Glu Cys Cys Gly Gln Lys Arg Ser Leu Ser			
45	50	55	
cg ^g gag gca ctg cag aag gat ctg gac aac ctc ttt gga cag cat	786		
Arg Glu Ala Leu Gln Lys Asp Leu Asp Asn Leu Phe Gly Gln His			
60	65	70	
ctt gca aag aaa atc atc tta aat gcc gtg ttt ggt ttc ata aac aac	834		
Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe Gly Phe Ile Asn Asn			
75	80	85	
cca aag ccc aag aaa cct ctc acg ctc tcc ctg cac ggg tgg aca ggc	882		
Pro Lys Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Thr Gly			
90	95	100	105
acc ggc aaa aat ttc gtc agc aag atc atc gca gag aat att tac gag	930		
Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala Glu Asn Ile Tyr Glu			
110	115	120	
ggt ggt ctg aac agt gac tat gtc cac ctg ttt gtg gcc aca ttg cac	978		
Gly Gly Leu Asn Ser Asp Tyr Val His Leu Phe Val Ala Thr Leu His			
125	130	135	
ttt cca cat gct tca aac atc acc ttg tac aag gat cag tta cag ttg	1026		
Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys Asp Gln Leu Gln Leu			
140	145	150	
tgg att cga ggc aac gtg agt gcc tgt gcg agg tcc atc ttc ata ttt	1074		
Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg Ser Ile Phe Ile Phe			
155	160	165	
gat gaa atg gat aag atg cat gca ggc ctc ata gat gcc atc aag cct	1122		
Asp Glu Met Asp Lys Met His Ala Gly Leu Ile Asp Ala Ile Lys Pro			
170	175	180	185
ttc ctc gac tat tat gac ctg gtg gat ggg gtc tcc tac cag aaa gcc	1170		
Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val Ser Tyr Gln Lys Ala			
190	195	200	
atg ttc ata ttt ctc agc aat gct gga gca gaa agg atc aca gat gtg	1218		
Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu Arg Ile Thr Asp Val			
205	210	215	
gct ttg gat ttc tgg agg agt gga aag cag agg gaa gac atc aag ctc	1266		
Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg Glu Asp Ile Lys Leu			
220	225	230	
aaa gac att gaa cac gcg ttg tct gtg tcg gtt ttc aat aac aag aac	1314		
Lys Asp Ile Glu His Ala Leu Ser Val Ser Val Phe Asn Asn Lys Asn			
235	240	245	

agt ggc ttc tgg cac agc agc tta att gac cg	g	ctc att gat tat	1362	
Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg	Asn	Leu Ile Asp Tyr		
250	255	260	265	
ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	cta	aaa atg tgt atc	1410	
Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His	Leu	Lys Met Cys Ile		
270	275	280		
cga gtg gaa atg cag tcc cga ggc tat gaa att	gat	gaa gac att gta	1458	
Arg Val Glu Met Gln Ser Arg Gly Tyr Glu Ile	Asp	Glu Asp Ile Val		
285	290	295		
agc aga gtg gct gag gag atg aca ttt ttc ccc	aaa	gag gag aga gtt	1506	
Ser Arg Val Ala Glu Glu Met Thr Phe Pro Lys	Glu	Glu Arg Val		
300	305	310		
ttc tca gat aaa ggc tgc aaa acg gtg ttc acc	aag	tta gat tat tac	1554	
Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr	Lys	Leu Asp Tyr Tyr		
315	320	325		
tac gat gat tgacagtcat gattggcagc cgaggactact gcctggagtt				1603
Tyr Asp Asp				
330				
ggaaaagaaa caacactcag tccttccaca cttccacccc cagctcctt cccttggaga	1663			
ggaatccagt gaatgttccct gtttgatgtg acaggaattc tccctggcat tggttccacc	1723			
cccttgggtgcc tgcagggccac ccagggacca cggggcgagga cgtgaagcct cccgaacacg	1783			
cacagaaggg aggagccagc tcccagccca ctcatcgag ggctcatgat tttttacaaa	1843			
ttatgtttta attccaaatgt tttctgtttc aaggaaggat gaataagttt tattgaaaat	1903			
gtggtaactt tattttaaat gatttttaac attatgagag actgctcaga ttcttaagtt	1963			
ttggccttgt gtgtgtt ttttttaagt tctcatcatt attacataga ctgtgaagta	2023			
tctttactgg aaatgagccc aagcacacat gcatggcatt tggttctgaa caggaggggca	2083			
tccctggggta tggctgttgc gcatgagcca gctctgtccc aggatggtcc cagcggatgc	2143			
tgccagggggc agtgaagtgt ttaggtgaag gacaagttagg taagaggacg ctttcaggca	2203			
ccacagataa gcctgaaaca gcctctccaa gggtttcac cttagcaaca atgggagctg	2263			
tgggagtgat tttggccaca ctgtcaacat ttgttagaac cagtcttttgg aaagaaaagt	2323			
atttccaact tggctacttgc cagtcactcc gtttgcaaa aggtggccct tcactgtcca	2383			
ttccaaatag cccacacgtg ctctctgtcg gattctaaat tatgtgaatt ttgccatatt	2443			
aaatcttcct catttataact attatttggt acgttcaatc agaatccccg aaacctcccta	2503			
taaagcttag ctgccccttc tgaggatgct gagaacggtg tctttcttta taaatgcaaa	2563			
tggctaccgt tttacaataa aattttgcac gtgc	2597			

<210> 2
 <211> 332
 <212> PRT
 <213> Homo sapien

<400> 2
 Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Ala Pro Ser
 1 5 10 15
 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
 20 25 30
 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
 35 40 45
 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95

Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160
 Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175
 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190
 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205
 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220
 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270
 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300
 Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
 305 310 315 320
 Thr Val Phe Thr Lys Leu Asp Tyr Tyr Asp Asp
 325 330

<210> 3
 <211> 3568
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (994) ... (1863)

<221> misc_feature
 <222> (1) ... (3568)
 <223> n = A, T, C or G

<400> 3
 tgatccgcct gcctcggcct cccaaagtgc tgggattaca ggcgtgagcg ccgcgcgg 60
 ccagcctgag acagttcgc tcttgcgcc caggctggag tgcagtgcga cgatctcgcc 120
 taactgcaac ctccgcctcc tgggttcaag agatttcct gcctcaacct ccgagtagct 180
 gggattacag gcgyscgcrc csmcrsccag ctttttttt ttttttttag acagttcgc 240
 tcttgcgcc aggctggagt gcagtgnnng anctcggcta actgcaactc cgctcctgg 300
 gttcaagaga ttctnctgcc tcaactcccg agtagctggg attatagng nccgcnacca 360
 caccatctaa ttttttgtat ttttagtaga gacggggttt cgcacgtga gcaggctgg 420
 ctcgaactcc tgacatcagg tgatccgcc gattcagctt cccaaagtgc tgggattaca 480
 ggcgtgagca cggcgcggc caaaaaaaaa aatattttt tttttttttt agatattttt 540
 tcactcttgt tgcccaaggct ggagtgaaat ggcgtgatct cggctcgcc tcccaaagtgc 600
 ctgggattac aggctgtaca ccngccgg sccgaaaaaa twtttttaaa agaaaaagg 660
 aaacaaaamag tctcctacac ctgcgrccac tcccaagaac gatggsacss cctccctctyc 720
 gnccctmacc aaccatggcc gnccnaagg gagtggggcg ggtctgcggg gcggaagtga 780
 cgsacgagag gaagtccgtc ctgcgcttgg ccgcggggcg cctggctcag tggcttctgc 840

gggcttcgag gagcgggatg ttgcgggctg ggtggctccg ggccggccgg cgctggcgct	900		
gctgctggcg gccccgagtttggcgagtttgcggccatc accgtggcc tagccatcg	960		
gcaggcgc catcaccgc tacctgtcct aca atg aca tct act gcc cgt tcg	1014		
Met Thr Ser Thr Ala Arg Ser			
1	5		
ccg agt gct gcc ggc gag gag cgg ccg ctc aac gct tcg gct ctc aag	1062		
Pro Ser Ala Ala Gly Glu Glu Arg Pro Leu Asn Ala Ser Ala Leu Lys			
10	15	20	
ctg gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg	1110		
Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val			
25	30	35	
att ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa	1158		
Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys			
40	45	50	55
cca ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt	1206		
Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe			
60	65	70	
gtc agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt	1254		
Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser			
75	80	85	
aac ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag	1302		
Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln			
90	95	100	
aag ata aaa ctg tac cag gac cag tta cag aag tgg atc cgc ggt aat	1350		
Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn			
105	110	115	
gtg agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa	1398		
Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys			
120	125	130	135
ttg cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac	1446		
Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr			
140	145	150	
gag cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc	1494		
Glu Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu			
155	160	165	
agc aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg	1542		
Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp			
170	175	180	
cgg gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct	1590		
Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro			
185	190	195	
gta ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac	1638		
Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His			
200	205	210	215

agt gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg 1686
 Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu
 220 225 230

 cct ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg 1734
 Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg
 235 240 245

 gcc cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag 1782
 Ala Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu
 250 255 260

 gaa atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc 1830
 Glu Met Thr Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly
 265 270 275

 tgc aag act gtg cag tcg cgg ctg gat ttc cac tgagctccta tccagatggg 1883
 Cys Lys Thr Val Gln Ser Arg Leu Asp Phe His
 280 285 290

 gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa 1943
 gaccgcttgc gggtttgcc tgtttgcacc ttagactttt gggatagaa tcttttttt 2003
 gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact 2063
 gcaacctccg ctcccggtt gagtgattct catgcctcag cctcccgagt agctggatt 2123
 acaggcatga gccactgtgc ccagctggga tatagaatct aagagttgat tgtggaaaac 2183
 acgtgaatct attgcgcga tttgtcattt agcaagatgg cagcagtcca gctgttctt 2243
 gcagctggag atgaactttt aaaaatcccc ttcacactta atgtactgac cgagacagaa 2303
 gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc 2363
 gcctcagaag ctacggtcac aactaaagga gtccaggac ttgctgcagg ctggggggca 2423
 ctgggtgggt ctcaccagca ggctgcgggg cactgttgc tcattggcca aaaacatcct 2483
 tttgctctgt ctcgtcttt acacagagtt cactgacttg aagtataactc agttaaaatc 2543
 ggggctggag gtgcagacgg tgcgtgaccc gaggatgtgg ccgtccccgc cgagcactct 2603
 ttagtctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct 2663
 gcagcagacc tggacagaca ggcgcctccc gcctgtccat cgctctagct gctaatacag 2723
 ccctggctgt ggaatccttc accgtctcag ctggatcag ccccagcctg ccttgggcc 2783
 atatctcagc ttggatctct gctagagttcc ccccaaccat atatcataga gttgaatcac 2843
 aatgagaccc ttggcttga attttagtgc ttgggtccca tggtagatg cttgttaaga 2903
 ctttataactt gggtaaatct ctcactttat tttttagaac catttggaaat ccttaggatgt 2963
 gcttggctgt gaaggatgac atggggccag actgaacaag tcagttgt gatcttaaat 3023
 gatgaaagta taggacgttgc ttattttaa aacaaggaa ggacacaaaa tggaaatgact 3083
 gccttagtcc tttctcagat actccttaaa acaattttt attgtttaaa tttgtggtaa 3143
 tacatggtca caaccgtgga tcaaacaagg tcagttcaaa gtggcaggcc cttaggtgtga 3203
 cctgatacca ccaccctttg tggcagcacc gggctggact gcccgtatcc ctgggacgtg 3263
 agacttagct tccagccagt gtgaatcatt gtatctgtct cataatcaca gcacagctgc 3323
 agacacaaca acgtgcagca ttttttacat aaaaatatgg tagaattaaat ttatgacatg 3383
 gaaatgcctt acgtggatc acacttagtc ttgaaaaaaa caccaagtg acgtttaaaa 3443
 ttttttagtac atatcctcaa attggagcta agttataactt cttttataac cttttgggcc 3503
 tctggtcgag agaagacaag atttctcta tttacagtga ggcaataaaat atgtttgcc 3563
 ccttt

<210> 4
 <211> 290
 <212> PRT
 <213> Homo sapien

<400> 4
 Met Thr Ser Thr Ala Arg Ser Pro Ser Ala Ala Gly Glu Glu Arg Pro
 1 5 10 15
 Leu Asn Ala Ser Ala Leu Lys Leu Asp Leu Glu Glu Lys Leu Phe Gly
 20 25 30

Gln His Leu Ala Thr Glu Val Ile Phe Lys Ala Leu Thr Gly Phe Arg
 35 40 45
 Asn Asn Lys Asn Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp
 50 55 60
 Ala Gly Thr Gly Lys Asn Phe Val Ser Gln Ile Val Ala Glu Asn Leu
 65 70 75 80
 His Pro Lys Gly Leu Lys Ser Asn Phe Val His Leu Phe Val Ser Thr
 85 90 95
 Leu His Phe Pro His Glu Gln Lys Ile Lys Leu Tyr Gln Asp Gln Leu
 100 105 110
 Gln Lys Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Asn Ser Val Phe
 115 120 125
 Ile Phe Asp Glu Met Asp Lys Leu His Pro Gly Ile Ile Asp Ala Ile
 130 135 140
 Lys Pro Phe Leu Asp Tyr Tyr Glu Gln Val Asp Gly Val Ser Tyr Arg
 145 150 155 160
 Lys Ala Ile Phe Ile Phe Leu Ser Asn Ala Gly Gly Asp Leu Ile Thr
 165 170 175
 Lys Thr Ala Leu Asp Phe Trp Arg Ala Gly Arg Lys Arg Glu Asp Ile
 180 185 190
 Gln Leu Lys Asp Leu Glu Pro Val Leu Ser Val Gly Val Phe Asn Asn
 195 200 205
 Lys His Ser Gly Leu Trp His Ser Gly Leu Ile Asp Lys Asn Leu Ile
 210 215 220
 Asp Tyr Phe Ile Pro Phe Leu Pro Leu Glu Tyr Arg His Val Lys Met
 225 230 235 240
 Cys Val Arg Ala Glu Met Arg Ala Arg Gly Ser Ala Ile Asp Glu Asp
 245 250 255
 Ile Val Thr Arg Val Ala Glu Glu Met Thr Phe Phe Pro Arg Asp Glu
 260 265 270
 Lys Ile Tyr Ser Asp Lys Gly Cys Lys Thr Val Gln Ser Arg Leu Asp
 275 280 285
 Phe His
 290

```
<210> 5
<211> 2072
<212> DNA
<213> Homo sapien
```

<220>
<221> CDS
<222> (43) ... (1038)

<400> 5
cgcgggtcggc gcgagaacaa gcaggggtggc gcggggtcgg gc atg aag ctg ggc 54
Met Lys Leu Gly
1

```

cg  gcc  gtg  ctg  ggc  ctg  ctg  ctg  ctg  gcg  ccg  tcc  gtg  gtg  cag  gcg  102
Arg  Ala  Val  Leu  Gly  Leu  Leu  Leu  Leu  Ala  Pro  Ser  Val  Val  Gln  Ala
      5           10           15           20

```

gtg gag ccc atc agc ctg gga ctg gcc ctg gcc ggc gtc ctc acc ggc 150
 Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly Val Leu Thr Gly
 25 30 35

tac atc tac ccg cgt ctc tac tgc ctc ttc gcc gag tgc tgc ggg cag	198																																																																																																																		
Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu Cys Cys Gly Gln																																																																																																																			
40	45	50		aag cgg agc ctt agc cgg gag gca ctg cag aag gat ctg gac gac aac	246	Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp Leu Asp Asp Asn		55	60	65		ctc ttt gga cag cat ctt gca aag aaa atc atc tta aat gcc gtg ttt	294	Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe		70	75	80		ggt ttc ata aac aac cca aag ccc aag aaa cct ctc acg ctc tcc ctg	342	Gly Phe Ile Asn Asn Pro Lys Pro Lys Pro Leu Thr Leu Ser Leu		85	90	95	100	cac ggg tgg aca ggc acc ggc aaa aat ttc gtc agc aag atc atc gca	390	His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala		105	110	115		gag aat att tac gag ggt ggt ctg aac agt gac tat gtc cac ctg ttt	438	Glu Asn Ile Tyr Glu Gly Leu Asn Ser Asp Tyr Val His Leu Phe		120	125	130		gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486	Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys		135	140	145		gat cag tta cag ttg tgg att cga ggc aac gtg agt gcc tgt gcg agg	534	Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg		150	155	160		tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582	Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile		165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275	
50																																																																																																																			
aag cgg agc ctt agc cgg gag gca ctg cag aag gat ctg gac gac aac	246																																																																																																																		
Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp Leu Asp Asp Asn																																																																																																																			
55	60	65		ctc ttt gga cag cat ctt gca aag aaa atc atc tta aat gcc gtg ttt	294	Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe		70	75	80		ggt ttc ata aac aac cca aag ccc aag aaa cct ctc acg ctc tcc ctg	342	Gly Phe Ile Asn Asn Pro Lys Pro Lys Pro Leu Thr Leu Ser Leu		85	90	95	100	cac ggg tgg aca ggc acc ggc aaa aat ttc gtc agc aag atc atc gca	390	His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala		105	110	115		gag aat att tac gag ggt ggt ctg aac agt gac tat gtc cac ctg ttt	438	Glu Asn Ile Tyr Glu Gly Leu Asn Ser Asp Tyr Val His Leu Phe		120	125	130		gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486	Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys		135	140	145		gat cag tta cag ttg tgg att cga ggc aac gtg agt gcc tgt gcg agg	534	Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg		150	155	160		tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582	Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile		165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275									
65																																																																																																																			
ctc ttt gga cag cat ctt gca aag aaa atc atc tta aat gcc gtg ttt	294																																																																																																																		
Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe																																																																																																																			
70	75	80		ggt ttc ata aac aac cca aag ccc aag aaa cct ctc acg ctc tcc ctg	342	Gly Phe Ile Asn Asn Pro Lys Pro Lys Pro Leu Thr Leu Ser Leu		85	90	95	100	cac ggg tgg aca ggc acc ggc aaa aat ttc gtc agc aag atc atc gca	390	His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala		105	110	115		gag aat att tac gag ggt ggt ctg aac agt gac tat gtc cac ctg ttt	438	Glu Asn Ile Tyr Glu Gly Leu Asn Ser Asp Tyr Val His Leu Phe		120	125	130		gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486	Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys		135	140	145		gat cag tta cag ttg tgg att cga ggc aac gtg agt gcc tgt gcg agg	534	Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg		150	155	160		tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582	Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile		165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																	
80																																																																																																																			
ggt ttc ata aac aac cca aag ccc aag aaa cct ctc acg ctc tcc ctg	342																																																																																																																		
Gly Phe Ile Asn Asn Pro Lys Pro Lys Pro Leu Thr Leu Ser Leu																																																																																																																			
85	90	95	100	cac ggg tgg aca ggc acc ggc aaa aat ttc gtc agc aag atc atc gca	390	His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala		105	110	115		gag aat att tac gag ggt ggt ctg aac agt gac tat gtc cac ctg ttt	438	Glu Asn Ile Tyr Glu Gly Leu Asn Ser Asp Tyr Val His Leu Phe		120	125	130		gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486	Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys		135	140	145		gat cag tta cag ttg tgg att cga ggc aac gtg agt gcc tgt gcg agg	534	Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg		150	155	160		tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582	Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile		165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																									
95	100																																																																																																																		
cac ggg tgg aca ggc acc ggc aaa aat ttc gtc agc aag atc atc gca	390																																																																																																																		
His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala																																																																																																																			
105	110	115		gag aat att tac gag ggt ggt ctg aac agt gac tat gtc cac ctg ttt	438	Glu Asn Ile Tyr Glu Gly Leu Asn Ser Asp Tyr Val His Leu Phe		120	125	130		gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486	Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys		135	140	145		gat cag tta cag ttg tgg att cga ggc aac gtg agt gcc tgt gcg agg	534	Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg		150	155	160		tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582	Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile		165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																	
115																																																																																																																			
gag aat att tac gag ggt ggt ctg aac agt gac tat gtc cac ctg ttt	438																																																																																																																		
Glu Asn Ile Tyr Glu Gly Leu Asn Ser Asp Tyr Val His Leu Phe																																																																																																																			
120	125	130		gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486	Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys		135	140	145		gat cag tta cag ttg tgg att cga ggc aac gtg agt gcc tgt gcg agg	534	Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg		150	155	160		tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582	Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile		165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																									
130																																																																																																																			
gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486																																																																																																																		
Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys																																																																																																																			
135	140	145		gat cag tta cag ttg tgg att cga ggc aac gtg agt gcc tgt gcg agg	534	Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg		150	155	160		tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582	Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile		165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																																	
145																																																																																																																			
gat cag tta cag ttg tgg att cga ggc aac gtg agt gcc tgt gcg agg	534																																																																																																																		
Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg																																																																																																																			
150	155	160		tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582	Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile		165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																																									
160																																																																																																																			
tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582																																																																																																																		
Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile																																																																																																																			
165	170	175	180	gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630	Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val		185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																																																	
175	180																																																																																																																		
gat gcc atc aag cct ttc ctc gac tat tat gac ctg gtg gat ggg gtc	630																																																																																																																		
Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val																																																																																																																			
185	190	195		tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678	Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu		200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																																																									
195																																																																																																																			
tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678																																																																																																																		
Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu																																																																																																																			
200	205	210		agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726	Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg		215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																																																																	
210																																																																																																																			
agg atc aca gat gtg gct ttg gat ttc tgg agg agt gga aag cag agg	726																																																																																																																		
Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg																																																																																																																			
215	220	225		gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774	Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val		230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																																																																									
225																																																																																																																			
gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774																																																																																																																		
Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val																																																																																																																			
230	235	240		ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822	Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg		245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																																																																																	
240																																																																																																																			
ttc aat aac aag aac agt ggc ttc tgg cac agc agc tta att gac cgg	822																																																																																																																		
Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg																																																																																																																			
245	250	255	260	aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870	Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His		265	270	275																																																																																																									
255	260																																																																																																																		
aac ctc att gat tat ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac	870																																																																																																																		
Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His																																																																																																																			
265	270	275																																																																																																																	
275																																																																																																																			

ct aaaaatgtatc cga gtg gaa atg cag tcc cga ggc tat gaa att	918																																																										
Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg Gly Tyr Glu Ile																																																											
280	285	290		gat gaa gac att gta agc aga gtg gct gag gag atg aca ttt ttc ccc	966	Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met Thr Phe Phe Pro		295	300	305		aaa gag gag aga gtt ttc tca gat aaa ggc tgc aaa acg gtg ttc acc	1014	Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr		310	315	320		aag tta gat tat tac tac gat gat tgacagtcat gattggcagc cgaggactact	1068	Lys Leu Asp Tyr Tyr Asp Asp		325	330	gcctggagtt ggaaaagaaa caacactca gtc tcc caca cttccacccc cagtccttt	1128	ccctggaga ggaatccagt gaatgtt cct gttt gatgtg acaggaat tc cctggcat	1188	tgttccacc ccctggtgcc tgcaggccac ccagggacca cggcgcagga cgtgaagcct	1248	cccgAACACG cacagaagga aggagccagc tccca gccc ctcatcgca ggctcatgtat	1308	ttttacaaa ttatgttttta attccaa gatgtg tttctgtttc aaggaaggat gaataagttt	1368	tattgaaaat gtggtaactt tatttaaaat gat ttttaac attatgagag actgctcaga	1428	tcttaagttt tgccctt gttgtgttt tttttaagt tctcatcatt attacataga	1488	ctgtgaagta tctttaactgg aatgagccc aagcacacat gcatggcatt ttttctgaa	1548	caggagggca tccctgggta tggctgtt gcatgagccca gctctgtccc aggatggtcc	1608	cagcggatgc tgccaggggc agtgaagtgt ttagtgaag gacaagttagg taagaggacg	1668	ccttcaggca ccacagataa gctgaaaca gctctccaa ggttttac cttagcaaca	1728	atgggagctg tggagtgat tttggccaca ctgtcaacat ttgtttagaac cagtctttt	1788	aaagaaaagt atttccaact tgcacttgc cagtcactcc gtttgcaaa aggtggccct	1848	tcactgtcca ttccaaatag cccacacgtg ctctgtctg gattctaaat tatgtgaatt	1908	ttgccatatt aaatcttcatt cattatact attattt gtt acgttcaatc agaatccccg	1968	aaaccttcata taaagcttag ctgccccttc tgaggatgct gagaacggtg tctttctta	2028	taaatgcaaa tggctaccgt tttacaataa aattttgcat gtgc	2072
290																																																											
gat gaa gac att gta agc aga gtg gct gag gag atg aca ttt ttc ccc	966																																																										
Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met Thr Phe Phe Pro																																																											
295	300	305		aaa gag gag aga gtt ttc tca gat aaa ggc tgc aaa acg gtg ttc acc	1014	Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr		310	315	320		aag tta gat tat tac tac gat gat tgacagtcat gattggcagc cgaggactact	1068	Lys Leu Asp Tyr Tyr Asp Asp		325	330	gcctggagtt ggaaaagaaa caacactca gtc tcc caca cttccacccc cagtccttt	1128	ccctggaga ggaatccagt gaatgtt cct gttt gatgtg acaggaat tc cctggcat	1188	tgttccacc ccctggtgcc tgcaggccac ccagggacca cggcgcagga cgtgaagcct	1248	cccgAACACG cacagaagga aggagccagc tccca gccc ctcatcgca ggctcatgtat	1308	ttttacaaa ttatgttttta attccaa gatgtg tttctgtttc aaggaaggat gaataagttt	1368	tattgaaaat gtggtaactt tatttaaaat gat ttttaac attatgagag actgctcaga	1428	tcttaagttt tgccctt gttgtgttt tttttaagt tctcatcatt attacataga	1488	ctgtgaagta tctttaactgg aatgagccc aagcacacat gcatggcatt ttttctgaa	1548	caggagggca tccctgggta tggctgtt gcatgagccca gctctgtccc aggatggtcc	1608	cagcggatgc tgccaggggc agtgaagtgt ttagtgaag gacaagttagg taagaggacg	1668	ccttcaggca ccacagataa gctgaaaca gctctccaa ggttttac cttagcaaca	1728	atgggagctg tggagtgat tttggccaca ctgtcaacat ttgtttagaac cagtctttt	1788	aaagaaaagt atttccaact tgcacttgc cagtcactcc gtttgcaaa aggtggccct	1848	tcactgtcca ttccaaatag cccacacgtg ctctgtctg gattctaaat tatgtgaatt	1908	ttgccatatt aaatcttcatt cattatact attattt gtt acgttcaatc agaatccccg	1968	aaaccttcata taaagcttag ctgccccttc tgaggatgct gagaacggtg tctttctta	2028	taaatgcaaa tggctaccgt tttacaataa aattttgcat gtgc	2072								
305																																																											
aaa gag gag aga gtt ttc tca gat aaa ggc tgc aaa acg gtg ttc acc	1014																																																										
Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr																																																											
310	315	320		aag tta gat tat tac tac gat gat tgacagtcat gattggcagc cgaggactact	1068	Lys Leu Asp Tyr Tyr Asp Asp		325	330	gcctggagtt ggaaaagaaa caacactca gtc tcc caca cttccacccc cagtccttt	1128	ccctggaga ggaatccagt gaatgtt cct gttt gatgtg acaggaat tc cctggcat	1188	tgttccacc ccctggtgcc tgcaggccac ccagggacca cggcgcagga cgtgaagcct	1248	cccgAACACG cacagaagga aggagccagc tccca gccc ctcatcgca ggctcatgtat	1308	ttttacaaa ttatgttttta attccaa gatgtg tttctgtttc aaggaaggat gaataagttt	1368	tattgaaaat gtggtaactt tatttaaaat gat ttttaac attatgagag actgctcaga	1428	tcttaagttt tgccctt gttgtgttt tttttaagt tctcatcatt attacataga	1488	ctgtgaagta tctttaactgg aatgagccc aagcacacat gcatggcatt ttttctgaa	1548	caggagggca tccctgggta tggctgtt gcatgagccca gctctgtccc aggatggtcc	1608	cagcggatgc tgccaggggc agtgaagtgt ttagtgaag gacaagttagg taagaggacg	1668	ccttcaggca ccacagataa gctgaaaca gctctccaa ggttttac cttagcaaca	1728	atgggagctg tggagtgat tttggccaca ctgtcaacat ttgtttagaac cagtctttt	1788	aaagaaaagt atttccaact tgcacttgc cagtcactcc gtttgcaaa aggtggccct	1848	tcactgtcca ttccaaatag cccacacgtg ctctgtctg gattctaaat tatgtgaatt	1908	ttgccatatt aaatcttcatt cattatact attattt gtt acgttcaatc agaatccccg	1968	aaaccttcata taaagcttag ctgccccttc tgaggatgct gagaacggtg tctttctta	2028	taaatgcaaa tggctaccgt tttacaataa aattttgcat gtgc	2072																
320																																																											
aag tta gat tat tac tac gat gat tgacagtcat gattggcagc cgaggactact	1068																																																										
Lys Leu Asp Tyr Tyr Asp Asp																																																											
325	330	gcctggagtt ggaaaagaaa caacactca gtc tcc caca cttccacccc cagtccttt	1128	ccctggaga ggaatccagt gaatgtt cct gttt gatgtg acaggaat tc cctggcat	1188	tgttccacc ccctggtgcc tgcaggccac ccagggacca cggcgcagga cgtgaagcct	1248	cccgAACACG cacagaagga aggagccagc tccca gccc ctcatcgca ggctcatgtat	1308	ttttacaaa ttatgttttta attccaa gatgtg tttctgtttc aaggaaggat gaataagttt	1368	tattgaaaat gtggtaactt tatttaaaat gat ttttaac attatgagag actgctcaga	1428	tcttaagttt tgccctt gttgtgttt tttttaagt tctcatcatt attacataga	1488	ctgtgaagta tctttaactgg aatgagccc aagcacacat gcatggcatt ttttctgaa	1548	caggagggca tccctgggta tggctgtt gcatgagccca gctctgtccc aggatggtcc	1608	cagcggatgc tgccaggggc agtgaagtgt ttagtgaag gacaagttagg taagaggacg	1668	ccttcaggca ccacagataa gctgaaaca gctctccaa ggttttac cttagcaaca	1728	atgggagctg tggagtgat tttggccaca ctgtcaacat ttgtttagaac cagtctttt	1788	aaagaaaagt atttccaact tgcacttgc cagtcactcc gtttgcaaa aggtggccct	1848	tcactgtcca ttccaaatag cccacacgtg ctctgtctg gattctaaat tatgtgaatt	1908	ttgccatatt aaatcttcatt cattatact attattt gtt acgttcaatc agaatccccg	1968	aaaccttcata taaagcttag ctgccccttc tgaggatgct gagaacggtg tctttctta	2028	taaatgcaaa tggctaccgt tttacaataa aattttgcat gtgc	2072																								
gcctggagtt ggaaaagaaa caacactca gtc tcc caca cttccacccc cagtccttt	1128																																																										
ccctggaga ggaatccagt gaatgtt cct gttt gatgtg acaggaat tc cctggcat	1188																																																										
tgttccacc ccctggtgcc tgcaggccac ccagggacca cggcgcagga cgtgaagcct	1248																																																										
cccgAACACG cacagaagga aggagccagc tccca gccc ctcatcgca ggctcatgtat	1308																																																										
ttttacaaa ttatgttttta attccaa gatgtg tttctgtttc aaggaaggat gaataagttt	1368																																																										
tattgaaaat gtggtaactt tatttaaaat gat ttttaac attatgagag actgctcaga	1428																																																										
tcttaagttt tgccctt gttgtgttt tttttaagt tctcatcatt attacataga	1488																																																										
ctgtgaagta tctttaactgg aatgagccc aagcacacat gcatggcatt ttttctgaa	1548																																																										
caggagggca tccctgggta tggctgtt gcatgagccca gctctgtccc aggatggtcc	1608																																																										
cagcggatgc tgccaggggc agtgaagtgt ttagtgaag gacaagttagg taagaggacg	1668																																																										
ccttcaggca ccacagataa gctgaaaca gctctccaa ggttttac cttagcaaca	1728																																																										
atgggagctg tggagtgat tttggccaca ctgtcaacat ttgtttagaac cagtctttt	1788																																																										
aaagaaaagt atttccaact tgcacttgc cagtcactcc gtttgcaaa aggtggccct	1848																																																										
tcactgtcca ttccaaatag cccacacgtg ctctgtctg gattctaaat tatgtgaatt	1908																																																										
ttgccatatt aaatcttcatt cattatact attattt gtt acgttcaatc agaatccccg	1968																																																										
aaaccttcata taaagcttag ctgccccttc tgaggatgct gagaacggtg tctttctta	2028																																																										
taaatgcaaa tggctaccgt tttacaataa aattttgcat gtgc	2072																																																										

<210> 6
<211> 332
<212> PRT
<213> Homo sapien

<400> 6	
Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Ala Pro Ser	
1 5 10 15	
Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly	
20 25 30	
Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu	
35 40 45	
Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp	
50 55 60	
Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu	
65 70 75 80	
Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Pro Leu	
85 90 95	
Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser	
100 105 110	
Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr	
115 120 125	
Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile	
130 135 140	
Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser	
145 150 155 160	

Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175
 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190
 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205
 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220
 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270
 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300
 Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
 305 310 315 320
 Thr Val Phe Thr Lys Leu Asp Tyr Tyr Asp Asp
 325 330

<210> 7
 <211> 2504
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (2) ... (799)

<400> 7
 g gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg att 49
 Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val Ile
 1 5 10 15

ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa cca 97
 Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys Pro
 20 25 30

ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt gtc 145
 Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe Val
 35 40 45

agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt aac 193
 Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser Asn
 50 55 60

ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag aag 241
 Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln Lys
 65 70 75 80

ata aaa ctg tac cag gac cag tta cag aag tgg atc cgc ggt aat gtg 289
 Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn Val
 85 90 95

agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa ttg	337																																																																																																																
Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys Leu																																																																																																																	
100	105	110		cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac gag	385	His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu		115	120	125		cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc agc	433	Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser		130	135	140		aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cg	481	Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg		145	150	155	160	gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta	529	Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val		165	170	175		ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	577	Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser		180	185	190		gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	625	Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro		195	200	205		ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673	Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala		210	215	220		cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721	Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu		225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779
110																																																																																																																	
cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac gag	385																																																																																																																
His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu																																																																																																																	
115	120	125		cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc agc	433	Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser		130	135	140		aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cg	481	Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg		145	150	155	160	gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta	529	Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val		165	170	175		ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	577	Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser		180	185	190		gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	625	Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro		195	200	205		ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673	Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala		210	215	220		cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721	Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu		225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779								
125																																																																																																																	
cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc agc	433																																																																																																																
Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser																																																																																																																	
130	135	140		aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cg	481	Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg		145	150	155	160	gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta	529	Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val		165	170	175		ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	577	Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser		180	185	190		gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	625	Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro		195	200	205		ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673	Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala		210	215	220		cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721	Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu		225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																
140																																																																																																																	
aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cg	481																																																																																																																
Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg																																																																																																																	
145	150	155	160	gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta	529	Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val		165	170	175		ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	577	Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser		180	185	190		gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	625	Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro		195	200	205		ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673	Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala		210	215	220		cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721	Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu		225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																								
155	160																																																																																																																
gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta	529																																																																																																																
Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val																																																																																																																	
165	170	175		ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	577	Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser		180	185	190		gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	625	Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro		195	200	205		ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673	Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala		210	215	220		cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721	Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu		225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																																
175																																																																																																																	
ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt	577																																																																																																																
Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser																																																																																																																	
180	185	190		gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	625	Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro		195	200	205		ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673	Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala		210	215	220		cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721	Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu		225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																																								
190																																																																																																																	
gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct	625																																																																																																																
Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro																																																																																																																	
195	200	205		ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673	Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala		210	215	220		cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721	Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu		225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																																																
205																																																																																																																	
ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc	673																																																																																																																
Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala																																																																																																																	
210	215	220		cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721	Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu		225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																																																								
220																																																																																																																	
cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa	721																																																																																																																
Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu																																																																																																																	
225	230	235	240	atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769	Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys		245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																																																																
235	240																																																																																																																
atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc	769																																																																																																																
Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys																																																																																																																	
245	250	255		aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819	Lys Thr Val Gln Ser Arg Leu Asp Phe His		260	265	gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879	gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939	gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999	gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059	acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119	acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179	gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239	gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299	gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359	ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419	tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479	ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539	tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599	gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659	ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719	atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																																																																								
255																																																																																																																	
aag act gtg cag tcg cgg ctg gat ttc cac tgagtccta tccagatggg	819																																																																																																																
Lys Thr Val Gln Ser Arg Leu Asp Phe His																																																																																																																	
260	265																																																																																																																
gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa	879																																																																																																																
gaccgctttg gggtttgcc tggttgacc tttagactttt gggatagaa tctttttttt	939																																																																																																																
gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtcaatcc tcaactcact	999																																																																																																																
gcaacctccg ctccccgtt gagtgattt catgcctcag cctcccggagt agctggatt	1059																																																																																																																
acaggcatga gccactgtgc ccagctggga tatagaatct aagagtttatgtggaaaac	1119																																																																																																																
acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtccat gctgttcttt	1179																																																																																																																
gcagctggag atgaactttt aaaaatcccc ttccacactta atgtactgac cgagacagaa	1239																																																																																																																
gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcacccgc	1299																																																																																																																
gcctcagaag ctacggcac aactaaagga gtccaggac ttgctgcagg ctggggggca	1359																																																																																																																
ctgggtgggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct	1419																																																																																																																
tttgccttgtt ctcgttctttt acacagagtt cactgacttg aagtataactc agttaaaatc	1479																																																																																																																
ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgccgc cgagcactct	1539																																																																																																																
tgtatctgagc tgacctgtgt gtgtgtgtgg ggggggggtgg ggccttcacc taagacctct	1599																																																																																																																
gcagcagacc tggacagaca ggccctccc gcctgtccat cgctctagct gctaatacag	1659																																																																																																																
ccctggctgtt ggaatccctt accgtctcag ctggatcatcg ccccagcctg ccttgggcc	1719																																																																																																																
atatctcagc ttggatctct gctagagtc ccccaaccat atatcataga gttgaatcac	1779																																																																																																																

aatgagaccc ttggcttga atttgagtcg ttggttccca tggtgagatg cttgttaaga 1839
 ctttatactt gggtaatct ctcactttat tttgtagaac catttgaat cctaggatgt 1899
 gcttgttctg gaaggatgac atgggcccag actgaacaag tcagcttgat gatcttaat 1959
 gatggaagta taggacgttg cttatTTaa aacaaggaa ggacacaaaaa tggatgact 2019
 gccttagtcc tttctcagat actccttaaa acaatTTTT attgtttaaa tttgtggtaa 2079
 tacatggtca caaccgtgga tcaaacaagg tcagtcataa gtggcaggc tcaggtgtga 2139
 cctgataccca ccaccctttg tggcagcacc gggctggact gccctgatcc ctgggacgtg 2199
 agacttagct tccagccagt gtgaatcatt gtatctgtct cataatcaca gcacagctgc 2259
 agacacaaca acgtgcagca tttttacat aaaaatatgg tagaattaat ttatgacatg 2319
 gaaatgcctt acgtgttac acacttagtc ttgaaaaaaa caccaaggtg acgtttaaaa 2379
 ttttagtac atatctcaa attggagcta agttatactt ctTTTataac ctTTTggca 2439
 tctggtcag agaagacaag atttctcta ttacagtga ggcaataaat atgtttgcca 2499
 ccttt 2504

<210> 8
 <211> 266
 <212> PRT
 <213> Homo sapien

<400> 8
 Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val Ile
 1 5 10 15
 Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys Pro
 20 25 30
 Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe Val
 35 40 45
 Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser Asn
 50 55 60
 Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln Lys
 65 70 75 80
 Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn Val
 85 90 95
 Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys Leu
 100 105 110
 His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu
 115 120 125
 Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser
 130 135 140
 Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg
 145 150 155 160
 Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val
 165 170 175
 Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser
 180 185 190
 Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro
 195 200 205
 Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala
 210 215 220
 Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu
 225 230 235 240
 Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys
 245 250 255
 Lys Thr Val Gln Ser Arg Leu Asp Phe His
 260 265

<210> 9
 <211> 332
 <212> PRT
 <213> Homo sapien

<400> 9
 Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Ala Pro Ser
 1 5 10 15
 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
 20 25 30
 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
 35 40 45
 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95
 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160
 Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175
 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190
 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205
 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220
 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270
 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300
 Thr Phe Phe Pro Lys Glu Glu Pro Val Phe Ser Asp Lys Gly Cys Lys
 305 310 315 320
 Thr Val Phe Thr Lys Leu Asp Tyr Tyr Asp Asp
 325 330

<210> 10
<211> 267
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (1)...(267)
<223> Xaa = any amino acid

<400> 10
 Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val
 1 5 10 15
 Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys
 20 25 30

Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe
 35 40 45
 Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser
 50 55 60
 Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln
 65 70 75 80
 Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn
 85 90 95
 Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys
 100 105 110
 Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr
 115 120 125
 Glu Gln Val Asp Gly Val Ser Tyr Xaa Lys Ala Ile Phe Ile Phe Leu
 130 135 140
 Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp
 145 150 155 160
 Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro
 165 170 175
 Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His
 180 185 190
 Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu
 195 200 205
 Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg
 210 215 220
 Ala Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu
 225 230 235 240
 Glu Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gln
 245 250 255
 Cys Lys Thr Val Gln Ser Arg Leu Asp Phe His
 260 265

<210> 11
 <211> 334
 <212> PRT
 <213> C. elegans

<400> 11
 Met Trp Met Lys Leu Asp Tyr Val Leu Leu Leu Phe His Leu Cys
 1 5 10 15
 Phe Val Asn Thr Glu Leu Ile Ser Val Ile Thr Gly Lys Ile Lys Asp
 20 25 30
 Ser Gly Thr Thr Ile Ala Ile Ser Ala Gly Ala Phe Trp Gly Leu Lys
 35 40 45
 Asp Arg Leu Lys Cys Tyr Leu Tyr Glu Cys Cys His Glu Pro Asp Val
 50 55 60
 Asn Phe Asn Tyr His Thr Leu Asp Ala Asp Ile Ala Asn Leu Leu Phe
 65 70 75 80
 Gly Gln His Leu Val Lys Asp Val Val Val Asn Ser Ile Lys Ser His
 85 90 95
 Trp Tyr Asn Glu Asn Pro Arg Lys Pro Leu Val Leu Ser Phe His Gly
 100 105 110
 Tyr Thr Gly Ser Gly Lys Asn Tyr Val Ala Glu Ile Ile Ala Asn Asn
 115 120 125
 Thr Phe Arg Leu Gly Leu Arg Ser Thr Phe Val Gln His Ile Val Ala
 130 135 140
 Thr Asn Asp Phe Pro Asp Lys Asn Lys Leu Glu Glu Tyr Gln Val Glu
 145 150 155 160

Leu Arg Asn Arg Ile Leu Thr Thr Val Gln Lys Cys Gln Arg Ser Ile
 165 170 175
 Phe Ile Phe Asp Glu Ala Asp Lys Leu Pro Glu Gln Leu Leu Gly Ala
 180 185 190
 Ile Lys Pro Phe Leu Asp Tyr Tyr Ser Thr Ile Ser Gly Val Asp Phe
 195 200 205
 Arg Arg Ser Ile Phe Ile Leu Leu Ser Asn Lys Gly Gly Gly Glu Ile
 210 215 220
 Ala Arg Ile Thr Lys Glu Gln Tyr Glu Ser Gly Tyr Pro Arg Glu Gln
 225 230 235 240
 Leu Arg Leu Glu Ala Phe Glu Arg Glu Leu Met Asn Phe Ser Tyr Asn
 245 250 255
 Glu Lys Gly Gly Leu Gln Met Ser Glu Leu Ile Ser Asn His Leu Ile
 260 265 270
 Asp His Phe Val Pro Phe Leu Pro Leu Gln Arg Glu His Val Arg Ser
 275 280 285
 Cys Val Gly Ala Tyr Leu Arg Lys Arg Gly Arg Gly Asp Leu Val Ser
 290 295 300
 Asn Val Asp Phe Val Glu Arg Val Leu Asn Ser Leu Gln Tyr Phe Pro
 305 310 315 320
 Glu Ser Ser Lys Ala Phe Ser Ser Ser Gly Cys Lys Arg Val
 325 330

<210> 12
 <211> 268
 <212> PRT
 <213> Homo sapien

<400> 12
 Leu Glu Cys Asp Leu Ala Gln His Leu Ala Gly Gln His Leu Ala Lys
 1 5 10 15
 Ala Leu Val Val Lys Ser Leu Lys Ala Phe Val Gln Asp Pro Ala Pro
 20 25 30
 Ser Lys Pro Leu Val Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys
 35 40 45
 Ser Tyr Val Ser Ser Leu Leu Ala Gln His Leu Phe Arg Asp Gly Leu
 50 55 60
 Arg Ser Pro His Val His His Phe Ser Pro Ile Ile His Phe Pro His
 65 70 75 80
 Pro Ser Arg Thr Glu Gln Tyr Lys Lys Glu Leu Lys Ser Trp Val Gln
 85 90 95
 Gly Asn Thr Ala Cys Glu Arg Ser Leu Phe Leu Phe Asp Glu Met Asp
 100 105 110
 Lys Leu Pro Pro Gly Leu Met Glu Val Leu Gln Pro Phe Leu Gly Pro
 115 120 125
 Ser Trp Val Val Tyr Gly Thr Asn Tyr Arg Lys Ala Ile Phe Ile Phe
 130 135 140
 Ile Ser Asn Ala Gly Gly Glu Cys Ile Asn Gln Val Ala Leu Glu Ala
 145 150 155 160
 Trp Arg Thr Asn Arg Asp Arg Glu Glu Ile Ser Leu Gln Glu Val Glu
 165 170 175
 Pro Val Ile Ser Arg Ala Val Met Asp Asn Pro Gln His Gly Phe Trp
 180 185 190
 Arg Ser Gly Ile Met Glu Glu His Leu Leu Asp Ala Val Val Pro Phe
 195 200 205
 Leu Pro Leu Gln Arg His His Val Arg His Cys Val Leu Asn Glu Leu
 210 215 220
 Ala Gln Leu Gly Leu Glu Pro Ala Arg Arg Trp Phe Arg Arg Cys Trp
 225 230 235 240

Thr	Asp	Thr	Tyr	Phe	Pro	Glu	Val	Glu	Gln	Leu	Phe	Ser	Ser	Asn	Gly
				245				250						255	
Cys	Lys	Thr	Val	Ala	Ser	Arg	Leu	Thr	Phe	Phe	Leu				
				260				265							

<210> 13
 <211> 177
 <212> PRT
 <213> Murine

<220>
 <221> VARIANT
 <222> (1) ... (177)
 <223> Xaa = Any Amino Acid

<400> 13
 Ala Ala Ala Leu His Gln Thr Leu Phe Ile Phe Asp Glu Ala Glu Lys
 1 5 10 15
 Leu His Pro Gly Leu Leu Glu Val Leu Gly Pro His Leu Glu Arg Arg
 20 25 30
 Ala Pro Glu Xaa Xaa Gly Leu Ser Leu Xaa Trp Thr Ile Phe Leu Phe
 35 40 45
 Leu Ser Asn Leu Arg Gly Asp Ile Ile Asn Glu Val Val Leu Lys Leu
 50 55 60
 Leu Lys Ala Gly Trp Ser Arg Glu Glu Ile Thr Met Glu His Leu Glu
 65 70 75 80
 Pro His Leu Gln Ala Glu Ile Val Asp Asp His Arg Gln Trp Leu Trp
 85 90 95
 His Ser Arg Leu Val Lys Glu Asn Leu Ile Asp Tyr Phe Ile Pro Phe
 100 105 110
 Leu Pro Leu Glu Tyr Arg His Val Arg Leu Cys Ala Arg Asp Ala Phe
 115 120 125
 Leu Ser Gln Glu Leu Leu Tyr Lys Glu Glu Thr Leu Asp Glu Ile Ala
 130 135 140
 Gln Met Met Val Tyr Val Pro Lys Glu Glu Gln Leu Phe Ser Ser Gln
 145 150 155 160
 Gly Cys Lys Ser Ile Xaa Gln Arg Ile Lys Leu Leu Pro Val Met Xaa
 165 170 175
 Gly

<210> 14
 <211> 214
 <212> PRT
 <213> Murine

<400> 14
 Glu Glu His Pro Leu Val Phe Leu Phe Leu Gly Ser Ser Gly Ile Gly
 1 5 10 15
 Lys Thr Glu Leu Ala Lys Gln Thr Ala Lys Tyr Met His Lys Asp Ala
 20 25 30
 Lys Lys Gly Phe Ile Arg Leu Asp Met Ser Glu Phe Gln Glu Arg His
 35 40 45
 Glu Val Ala Lys Phe Ile Gly Ser Pro Arg Gly Tyr Ile Gly His Glu
 50 55 60
 Glu Gly Gly Gln Leu Thr Lys Lys Leu Lys Gln Cys Pro Asn Ala Val
 65 70 75 80

Val Leu Phe Asp Glu Val Asp Lys Ala His Pro Asp Val Leu Thr Ile
 85 90 95
 Met Leu Gln Leu Phe Asp Glu Gly Arg Leu Thr Asp Gly Lys Gly Lys
 100 105 110
 Thr Ile Asp Cys Lys Asp Ala Ile Phe Ile Met Thr Ser Asn Val Ala
 115 120 125
 Ser Asp Glu Ile Ala Gln His Ala Leu Gln Leu Arg Gln Glu Ala Leu
 130 135 140
 Glu Met Ser Arg Asn Arg Ile Ala Glu Asn Leu Gly Asp Val Gln Met
 145 150 155 160
 Ser Asp Lys Ile Thr Ile Ser Lys Asn Phe Lys Glu Asn Val Ile Arg
 165 170 175
 Pro Ile Leu Lys Ala His Phe Arg Arg Asp Glu Phe Leu Gly Arg Ile
 180 185 190
 Asn Glu Ile Val Tyr Phe Leu Pro Phe Cys His Ser Glu Leu Ile Gln
 195 200 205
 Leu Val Asn Lys Glu Leu
 210

<210> 15
 <211> 185
 <212> PRT
 <213> Unknown

<220>
 <223> Soybean

<400> 15
 Pro Gln Gln Pro Thr Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val
 1 5 10 15
 Gly Lys Thr Glu Leu Ala Lys Ala Leu Ala Glu Gln Leu Phe Asp Asn
 20 25 30
 Glu Asn Gln Leu Val Arg Ile Asp Met Ser Glu Tyr Met Glu Gln His
 35 40 45
 Ser Val Ser Arg Leu Ile Gly Ala Pro Pro Gly Tyr Val Gly His Glu
 50 55 60
 Glu Gly Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Ser Val
 65 70 75 80
 Val Leu Phe Asp Glu Val Glu Lys Ala His Thr Ser Val Phe Asn Ile
 85 90 95
 Leu Leu Gln Val Leu Asp Asp Gly Arg Leu Thr Asp Gly Gln Gly Arg
 100 105 110
 Thr Val Asp Phe Arg Asn Thr Val Ile Ile Met Thr Ser Asn Leu Gly
 115 120 125
 Ala Glu His Leu Leu Ser Gly Ser Gln Lys Cys Thr Met Gln Val Ala
 130 135 140
 Arg Asp Arg Val Met Glu Gln Glu Arg Arg Gln Phe Arg Pro Glu Leu
 145 150 155 160
 Leu Asn Arg Leu Asp Glu Ile Val Val Phe Asp Pro Leu Ser His Asp
 165 170 175
 Gln Leu Arg Lys Val Ala Arg Leu Met
 180 185

<210> 16
 <211> 194
 <212> PRT
 <213> Homo sapien

<400> 16

Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly
 1 5 10 15
 Lys Asn Phe Val Ser Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly
 20 25 30
 Leu Asn Ser Asp Tyr Val His Leu Phe Val Ala Thr Leu His Phe Pro
 35 40 45
 His Ala Ser Asn Ile Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile
 50 55 60
 Arg Gly Asn Val Ser Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu
 65 70 75 80
 Met Asp Lys Met His Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu
 85 90 95
 Asp Tyr Tyr Asp Leu Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe
 100 105 110
 Ile Phe Leu Ser Asn Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu
 115 120 125
 Asp Phe Trp Arg Ser Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp
 130 135 140
 Ile Glu His Ala Leu Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly
 145 150 155 160
 Phe Trp His Ser Ser Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val
 165 170 175
 Pro Phe Leu Pro Leu Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val
 180 185 190
 Glu Met

<210> 17
 <211> 194
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(194)
 <223> Xaa = Any Amino Acid

<400> 17
 Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly
 1 5 10 15
 Lys Asn Phe Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly
 20 25 30
 Leu Lys Ser Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro
 35 40 45
 His Glu Gln Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile
 50 55 60
 Arg Gly Asn Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu
 65 70 75 80
 Met Asp Lys Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu
 85 90 95
 Asp Tyr Tyr Glu Gln Val Asp Gly Val Ser Tyr Xaa Lys Ala Ile Phe
 100 105 110
 Ile Phe Leu Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu
 115 120 125
 Asp Phe Trp Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp
 130 135 140
 Leu Glu Pro Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly
 145 150 155 160

Leu Trp His Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile
 165 170 175
 Pro Phe Leu Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala
 180 185 190
 Glu Met

<210> 18
 <211> 192
 <212> PRT
 <213> C. elegans

<400> 18
 Pro Arg Lys Pro Leu Val Leu Ser Phe His Gly Tyr Thr Gly Ser Gly
 1 5 10 15
 Lys Asn Tyr Val Ala Glu Ile Ile Ala Asn Asn Thr Phe Arg Leu Gly
 20 25 30
 Leu Arg Ser Thr Phe Val Gln His Ile Val Ala Thr Asn Asp Phe Pro
 35 40 45
 Asp Lys Asn Lys Leu Glu Glu Tyr Gln Val Glu Leu Arg Asn Arg Ile
 50 55 60
 Leu Thr Thr Val Gln Lys Cys Arg Ser Ile Phe Ile Phe Asp Glu Ala
 65 70 75 80
 Asp Lys Leu Pro Glu Gln Leu Leu Gly Ala Ile Lys Pro Phe Leu Asp
 85 90 95
 Tyr Tyr Ser Thr Ile Ser Gly Val Asp Phe Arg Arg Ser Ile Phe Ile
 100 105 110
 Leu Leu Ser Asn Lys Gly Gly Glu Ile Ala Arg Ile Thr Lys Glu
 115 120 125
 Gln Tyr Glu Ser Gly Tyr Pro Arg Glu Gln Leu Arg Leu Glu Ala Phe
 130 135 140
 Glu Arg Glu Leu Met Asn Phe Ser Tyr Asn Glu Lys Gly Leu Gln
 145 150 155 160
 Met Ser Glu Leu Ile Ser Asn His Leu Ile Asp His Phe Val Pro Phe
 165 170 175
 Leu Pro Leu Gln Arg Glu His Val Arg Ser Cys Val Gly Ala Tyr Leu
 180 185 190

<210> 19
 <211> 194
 <212> PRT
 <213> Homo sapien

<400> 19
 Pro Ser Lys Pro Leu Val Leu Ser Leu His Gly Trp Thr Gly Thr Gly
 1 5 10 15
 Lys Ser Tyr Val Ser Ser Leu Leu Ala Gln His Leu Phe Arg Asp Gly
 20 25 30
 Leu Arg Ser Pro His Val His His Phe Ser Pro Ile Ile His Phe Pro
 35 40 45
 His Pro Ser Arg Thr Glu Gln Tyr Lys Lys Glu Leu Lys Ser Trp Val
 50 55 60
 Gln Gly Asn Leu Thr Ala Cys Glu Arg Ser Leu Phe Leu Phe Asp Glu
 65 70 75 80
 Met Asp Lys Leu Pro Pro Gly Leu Met Glu Val Leu Gln Pro Phe Leu
 85 90 95
 Gly Pro Ser Trp Val Val Tyr Gly Thr Asn Tyr Arg Lys Ala Ile Phe
 100 105 110
 Ile Phe Ile Ser Asn Ala Gly Gly Glu Gln Ile Asn Gln Val Ala Leu
 115 120 125

Glu Ala Trp Arg Thr Asn Arg Asp Arg Glu Glu Ile Ser Leu Gln Glu
 130 135 140
 Val Glu Pro Val Ile Ser Arg Ala Val Met Asp Asn Pro Gln His Gly
 145 150 155 160
 Phe Trp Arg Ser Gly Ile Met Glu Glu His Leu Leu Asp Ala Val Val
 165 170 175
 Pro Phe Leu Pro Leu Gln Arg His His Val Arg His Cys Val Leu Asn
 180 185 190
 Glu Leu

<210> 20
 <211> 128
 <212> PRT
 <213> Murine

<220>
 <221> VARIANT
 <222> (1)...(128)
 <223> Xaa = Any Amino Acid

<400> 20
 Ala Ala Ala Leu His Gln Thr Leu Phe Ile Phe Asp Glu Ala Glu Lys
 1 5 10 15
 Leu His Pro Gly Leu Leu Glu Val Leu Gly Pro His Leu Glu Arg Arg
 20 25 30
 Ala Pro Glu Xaa Xaa Gly Leu Ser Leu Xaa Trp Thr Ile Phe Leu Phe
 35 40 45
 Leu Ser Asn Leu Arg Gly Asp Ile Ile Asn Glu Val Val Leu Lys Leu
 50 55 60
 Leu Lys Ala Gly Trp Ser Arg Glu Glu Ile Thr Met Glu His Leu Glu
 65 70 75 80
 Pro His Leu Gln Ala Glu Ile Val Asp Asp His Arg Gln Trp Leu Trp
 85 90 95
 His Ser Arg Leu Val Lys Glu Asn Leu Ile Asp Tyr Phe Ile Pro Phe
 100 105 110
 Leu Pro Leu Glu Tyr Arg His Val Arg Leu Cys Ala Arg Asp Ala Phe
 115 120 125

<210> 21
 <211> 253
 <212> DNA
 <213> Homo sapien

<400> 21
 cctgaaatac aaacacctaa aatgtgtat ccgagtggaa atgcagtccc gaggctatga 60
 aattgatgaa gacattgtaa gcagagtggc tgaggagatg acattttcc ccaaagagga 120
 gagagtttc tcagataaaag gctgaaaaac ggtgttcacc aagtttagatt attactacga 180
 tgattgacag tcatgattgg cagccggagt cactgcctgg agttggaaag aaacaacact 240
 cagtccttcc acc 253

<210> 22
 <211> 253
 <212> DNA
 <213> Homo sapien

<400> 22
 ggaccttatg tttgtggatt tttacacata ggctcacctt tacgtcaggg tccgatactt 60

taactacttc tgtaacattc gtctcaccga ctcctctact gtaaaaaggg gtttctcctc 120
 tctcaaaaga gtctatttc gacgtttgc caccaagtgg ttcaatctaa taatgatgct 180
 actaactgtc agtactaacc gtcggcctca gtgacggacc tcaaccttc tttgttgtga 240
 gtcaggaagg tgg 253

<210> 23
 <211> 7
 <212> PRT
 <213> Homo sapien

<400> 23
 Phe Phe Thr Met Glu Ala Val
 1 5

<210> 24
 <211> 21
 <212> DNA
 <213> Homo sapien

<400> 24
 gtggctgaga tgacatttt c 21

<210> 25
 <211> 24
 <212> DNA
 <213> Homo sapien

<400> 25
 gtggctgagg agatgacatt ttcc 24

<210> 26
 <211> 8
 <212> PRT
 <213> Homo sapien

<400> 26
 Phe Phe Thr Met Glu Glu Ala Val
 1 5

<210> 27
 <211> 205
 <212> DNA
 <213> Synthetic

<400> 27
 cctggaatac aaacacctaa aatgtgtat ccgagtgaa atgcagtccc gaggctatga 60
 aattgtgaa gacattgtaa gcagagtggc tgaggagatg acattttcc ccaaagagga 120
 gagagtttc tcagataaag gctgaaaac ggtgttccacc aagtttagatt attactacga 180
 tgattgacag tcatgattgg cagcc 205

<210> 28
 <211> 19
 <212> DNA
 <213> Synthetic

<400> 28
 cctggaatac aaacaccta 19

<210> 29

<211> 20
 <212> DNA
 <213> Synthetic

<400> 29
 ggctgccaaat catgactgtc

20

<210> 30
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 30
 gcaaaaacagg gctttgtacc g

21

<210> 31
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 31
 agtagagacg cgggttagatg

20

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 32
 gcgtctctac tgcctttcg

20

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 33
 atgccctggc cctagttcag

20

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 34

ggttcgcaa ggtgcttggaa	20
<210> 35	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 35	20
gggattccaa acttccatcc	
<210> 36	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 36	20
tccatgggt tggtaggaac	
<210> 37	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 37	22
ggtgacagag taaaactatc tg	
<210> 38	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 38	20
gacccccagt agacgtttgt	
<210> 39	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Synthetic oligonucleotide	
<400> 39	21
gtaaaaaaatc atgagccctg c	
<210> 40	
<211> 20	
<212> DNA	

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 40

ccagagttag tgagcaggtc

20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 41

gaagcgtaa ggacctccac

20

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 42

atctatctct gccaaattcc ac

22

<210> 43

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 43

gtcctggtaa acaaagtgt g

21

<210> 44

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 44

tggggttact ctatgttggt c

21

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 45
 ctagcacagt atgccctaag 20

<210> 46
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 46
 tgaggaatgt gctgagggtc 20

<210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 47
 gctgtctcct accccatctg 20

<210> 48
 <211> 283
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 1

<221> misc_feature
 <222> (1)...(283)
 <223> n = A,T,C or G

<400> 48
 gtaggctggg gcgggggctg gaggctgggg ctggggctgg ggctgggcga tggcactagg 60
 gctgaactag gaccaggcga tggagaatgg aggatggagg ccgggggatg gcaccaggc 120
 cgggcttagga ctagggctgg agcggggcct gggggctggg gctgggcgt ggcactaggg 180
 cgggttgggg ctggggctgg ggctggggga tggagcgggg ccgggggctg ggggtgggc 240
 tggggatcg actagggtctg gnttaggacc aggccgttgg cat 283

<210> 49
 <211> 375
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 1

<221> misc_feature
 <222> (1)...(375)
 <223> n = A,T,C or G

<400> 49
 ggatggtggga tggaggctgg gggatggcag tagggccggg ctaggactgg ggctggagcg 60
 gagtttgggg ctggggctca ggagcggggg ctggggctgg ggctggggct gggggatggc 120
 actagggtcag gccggggtag gggtcacatc ccaggaggc cgggctggc agagctgagt 180

ccgcggggggc cgaccccg aagccaagcn gccggcctgc aggatgaggc ctggctcctc 240
 gccatgacc acagacgtgc cagacttaag tacggagacc tgaggagcca ggctgcagtt 300
 ggcctacttt ncnctaagct ggggtggac cagtggtaac ctccctccgaa gtgggttctg 360
 ctcttctag cctag 375

<210> 50
 <211> 439
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 1

<221> misc_feature
 <222> (1)...(439)
 <223> n = A,T,C or G

<400> 50
 ccactgccac tgccaccagt ttgcacccct aaccctgtt ctgctcctcc caccggagg 60
 cagagccgg 120
 cggaaac agtttggtcc ctcctggtc gctgcggaaag agtctcacca 120
 tccttctgtc tccgtagcta gaaaggaggc agaaccaca ttccggaggga ggttaccact 180
 ggtccacccc cagcttagcg caaagttaggc caacctgcac gcctggnnct cctcaggntc 240
 tgcttactta agtctggcag ctctnnntca tggccgaggt agccaggctc atcctgcagg 300
 nnccngccnn ttgncttncc ggggtntcgn nncccccgtac tcagctcgac cagccggcct 360
 ctggatgtga cctaccgctg ctatgtcattt ccagccagcc agccagccgt ctagccagcc 420
 aactgcttag ccagttctag 439

<210> 51
 <211> 368
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 1

<221> misc_feature
 <222> (1)...(368)
 <223> n = A,T,C or G

<400> 51
 caaagccaat caggagtggg gaagaaacac ggcaaaatgt agccacattt acagccata 60
 aganagccag caaagccgtc tagcctccaa gcacccctgcg aaacctcaag tactgcggtc 120
 tggtaagctc ctggcccaaga gggacggcg gtccaggng ccctccctt gctggctctg 180
 cctattctaa agccctggcc cgnctccttc ccgaaaagcc ccttggtgcc actgccactg 240
 ccaccanttt gcnnccctac ccctgtntcgt ctccctccac cccaaaggcag atgcggnnng 300
 ngaaaggaaa canttggtc cctcctggtc ggctcgngga agactcctca ccatccttcc 360
 tggatgtga 368

<210> 52
 <211> 400
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 2

<400> 52
 gaatattttac gaggggtggtc tgaacagtga ctatgtccac ctgtttgtgg ccacattgct 60
 ctttccacat gcttcaaaca tcaccttgcg caaggcaagg atgaaatgtt ggaatccctt 120
 cctggatgtc atcgggtttg gggctctttt gttgtggat gagatttggg agttctatgt 180

```
tggaaatgggt gagcccgaa aacgggtcat gtctcagttc cccttggaaa ggtgtagaag 240
ttaagagttt gagatgcgtg gagcagttaa taccatcaa gctttgtgtt gggttctgaa 300
aatcggtcca gtgagttatgt agggtcatgg gatttttagag gtggacatga tcaaattccat 360
cttaqaqatc aacacatctc actcattttt attttcttat 400
```

<210> 53
<211> 418
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 2

```
<221> misc_feature
<222> (1)...(418)
<223> n = A,T,C or G
```

```

<400> 53
tttggagtga gacaggactg gttcagggtc ccagctctgc cacatatagt ctggggcaag 60
tggagtaagc gctctctgtg cctcagttcc ctcatctgt aaatgagaac gatagtgc 120
actccatggg gttggtagga acaaagaaga ttttgggcat gtaaaagtct tagtgccgag 180
tgcacagtgg tctgttaagtg aagctgcgt tcttagtgtt agaaggagct gattgtatggc 240
cctggctgag aactttgtgt tcgcttttc cnntttaat tcagatcag ttacagtgt 300
ggattcgagg caacgtgagt gcctgtgcga gttccatctt catattgtat gaaatggata 360
agatgcatgc aggcctcata gatgcncntca anccttcctt cgactattat gacctgg 418

```

<210> 54
<211> 198
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 3

<400> 54
ctcgacttatt atgacctgggt ggatggggtc tcctaccaga aagccatgtt catatttctc 60
aggtaaggtc agggcttagga catgatggat gggcccccagc cccaaaggctc tgagctccag 120
gagaaaaaccc tgtccttacc cactgggatt gttttgcagc aatgtctggag cagaaaggat 180
cacagatgtg tttggatt 198

<210> 55
<211> 536
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 4

```
<221> misc_feature  
<222> (1)...(536)  
<223> n = A,T,C or G
```

```

<400> 55
gtctgtgtcg gttttcaata acaagaacag gtgagtaggg ccatccaccg ccagtcac 60
ctggttccta atcctgcacc ctaagtgtta aaagcatca ggtcaactgtc agcatcac 120
gggagctggg tagaaaagaaa tggagattct cagtcacccctt ccgagtcatg agggaaatct 180
ttgctgatga actccaggtt acttttatga acactaatgt ttgacaagtg ctgttttatt 240
tttatttttc agatagtttt actctgtcac cttaggctgaa gtgcagtgcc gtaaccttgc 300
ctcaactgcaa cctctgcctc ccgggctcaa gcgattcttg tgcctcagcc tcctgagtag 360
ctgggattac aggtgcacac catgccccaa cnaatatttt gtatTTTtag tagaganggg 420

```

gcccgtnca tgttaaccag gctggtctt aactnttacc tcaggtgagt ccnccacctc 480
 ggctcccaa agtgctggta ttacaggcgt gagccactgt gtctcagctt atttt 536

<210> 56
 <211> 1302
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 4

<221> misc_feature
 <222> (1)...(1302)
 <223> n= A,T,C or G; m= A,or C; r= G,or A; w= A,or T; y= C,or T

<400> 56
 gccactccaa gctaccatct gagattgttt cctgccc tag agtggtaaag gcgtgaggc 60
 cgtctgcctt cagctgtgtc cccaggcca gggcgtgcct ggcaacanna gcagccctct 120
 gagaaccagc ctcccacgtg agttcatgt agnaagacag cccctcggtc ccattcagtg 180
 gtgggtctg ttcttccctt ggcmataagc tccactctgy mrtcagccam acatttattg 240
 agtaccagtt gttggcaaag cactgttggg catgaaaagc attaaccagg tgaatgagga 300
 ggagcttggg ttgggacgga gcmcaraaw tacatggcag accagaagga aatcagctca 360
 agtagaaara cacgcacatggg ctcgtggcg acgcacgtgt tgctgtgtca tctggggctg 420
 ggaggaagtg tcctggatca ggagttccag gagcccagga ggagtggacg ggtcagtgc 480
 gagccagccc gcaatcaggg gaagaaaaaca cggccaaggc caggccttca cggggagccc 540
 agcgtgggt gcacatctgc actctccagg ctatgtttgg tgcccacatg ctctgcagg 600
 tctgggcact gtggcagcgg cagcaggctt ccctgttgct agtccagctg ctgaaactcc 660
 agggagagtc aaaaagttcc caaatacaga ggcgtggctg gtatgccttc ccggaaattc 720
 ttcttgcttc ccgcttctg tggactctg cttcccccac tctgccttc tgctgttcc 780
 tggggcccaag gaccttttc ccatcttcga tctcttaagt cataccttgg gaggcctccc 840
 ccagcccgcc gtgtaaagag ggctgtcaca gttctgtctg tcacagaagc attacaatgt 900
 gcaggtgcctt gttaacatct gccttccca ctgatctgga gtcacaaag ggagagggca 960
 cacccagtag gtatgtgtgg gatggatagg aggggtggatg acacccagta gatgtgtatg 1020
 ggtatggatg gagggtggat gacacccagt aggtgtgtat gggatggatg ggagggtgg 1080
 tgacccctag tagatgtggg ggggggtgggt gggtagccccc cagtaggtgt gtgtggcatg 1140
 gataggtgac ccccaactaga ctgttgcgg acggatggga gggtaggtaa gtgacccccc 1200
 ggaggcgtct atagggcagg tgggtggatg tggatgaaca gcaccccttgc tcttctccc 1260
 aggtggcttc tggcacagca gtttaattga ccggaaacctc at 1302

<210> 57
 <211> 240
 <212> DNA
 <213> Unknown

<220>
 <223> TORB intron 1-5'

<221> misc_feature
 <222> (1)...(240)
 <223> n = A,T,C or G

<400> 57
 ggagcggccg ctcaacgctt cgggtacggc gcgcgcgcga gctgtgggtc ggcgtgcgg 60
 ggggcgcggg ggcgcggggg cgcggaggga cggcctcggt ggcgcctggc acggaccggg 120
 cccgtggcat ctagacggcg gtggtcccag ctgggggtggg cggggagcgg atggggcggc 180
 cccggaaaccg ttgcnggaa cgcagaagcn gtgccttgc acactctcag atcgtgnngc 240

<210> 58
 <211> 310

```

<212> DNA
<213> Unknown

<220>
<223> TORB intron 1-3'

<221> misc_feature
<222> (1)...(310)
<223> n = A,T,C or G

<400> 58
gggacccaaag gacgtccgtc gttcccaccc accctaatacg ttgcgcngtc ngttcgctac 60
ccagtagaga gacttactta cnngtnnacg gaaggaatacg tctggggcgtt cgcaattcct 120
ggaggtgtat tagaactttc accgttagcaa actgacggag ccgggatccc acaccgcctg 180
tgggnncgac acgggaccta ttgacacgaa gaacgaaacn gtcgattcgtt tcacgacgca 240
acgactacgt aaaaattcca gacaaagaga gaaacaagac cccgacaaga acgtcgagag 300
ttcgacctaa 310

<210> 59
<211> 401
<212> DNA
<213> Unknown

<220>
<223> TORB intron 2-5'

<221> misc_feature
<222> (1)...(401)
<223> n = A,T,C or G

<400> 59
caggaacaac aaaaatcccc aaaaaaccact gaccctttcc ttacacggct gggctggcac 60
aggcaagaat ttgtcagtn aatttgtggc tgaaaaatctt caccggaaaag gtctgaagag 120
taactttgtc cacctgtttg tatcgactct gcacccctt catgagcaga agataaaaact 180
gtaccaggca agagaacccg ctattatctc gtctgcaggc cagtcggact ggtccgggtg 240
acctgctcac taactctggc ctctgcttct ctttcccttg tggcgtgtt gccccggct 300
ccactgagtt aaggcacact tagtccaggt agttacaaag ctctcctaca acatttctta 360
cttgggttcca aaacagtcca gtggggtagg ggatgttatt t 401

<210> 60
<211> 238
<212> DNA
<213> Unknown

<220>
<223> TORB intron 2-3'

<400> 60
ttctgttaact ggtccctggac caaccatgaa agaagaaaaca ggatgcgaag ctcaaaggac 60
tgccaccaaga ggccgcgcagg ctccatctgc tcctcatgca ctgaggacg aggtcagacg 120
tcttagaaatg gcaccctcac ccccaactcgc taggttagcag ctttctaaa accttatctc 180
taaaaaatggg aaattggcag agatagatgc taaaatgcag agaagttttt ccttaactc 238

<210> 61
<211> 391
<212> DNA
<213> Unknown

<220>
<223> TORB intron 3-5'

```

<221> misc_feature
 <222> (1)...(391)
 <223> n = A,T,C or G

<400> 61
 gggatcattg acgcaatcaa gccgtttcta gactactacg agcaggttga cggagtgtct 60
 taccgcaaag ccatcttcat ctttctcagg tcagcggag gcgggtttttt gggcacaca 120
 agcccttcat tctctcaatg ataaaatgag gtcctgagga ccatcagcac tttgtttacc 180
 aggacgaaag tgcctgcttgcacaaggcca cttacctact gctttacttt tccttgccca 240
 gtcatcagca tggcacacag tgtgggttgttggaaatgaac taaagaaata atcactggga 300
 caggcgcgggttggctcacacc tgtcaatccn agcactttgg gnaggcatgg cgggcggatc 360
 acaggagatc gagacatctg ctaacatgnt g 391

<210> 62
 <211> 373
 <212> DNA
 <213> Unknown

<220>
 <223> TORB intron 3-3'

<221> misc_feature
 <222> (1)...(373)
 <223> n = A,T,C or G

<400> 62
 gtaagacaca gagtcctttt tnttttttag accgagtntc attnttggcc cnangctgg 60
 agtcaatgg catgatctcg gtcgtctgca acctccaccc cccgrrtca aacgattctc 120
 ccacccatgc ctcctatgtt gctgggatata cagncatgca ccaccattag cctggctaat 180
 ttttgggtttt ttagtagaga tgggggtact ctatgttggt caggctggcc ttgaactccc 240
 gacctcaggat gatctacctg ctcggccctc ccaaagtgc gggattacag ccatgagcna 300
 ccacnscnan cagacncaga agtcttaata tgtgattttt atctttattt ctctggcaaa 360
 ctcagcaatg cag 373

<210> 63
 <211> 310
 <212> DNA
 <213> Unknown

<220>
 <223> TORB intron 4'

<221> misc_feature
 <222> (1)...(310)
 <223> n = A,T,C or G

<400> 63
 gtgagtccac caggtaaaag gagccctta actgtccagc agtgagccgt ctgctttc 60
 attgagtgtt tgcacaaagc cacaggatcc cactggattt cctcaactttg ctaaagtca 120
 gaattttctt agggcataact gtgctagaaa ccagtggatg agtgcgcagc tgagtccctcg 180
 atgggcttgt tgcacactga caagagacnc tctcaagggg tacggacatg aggaatgtgc 240
 tgagggtcgg gactggagct tggccaggtg gcgggtggcaggaaaccc agctgtgtct 300
 tggctgcag 310

<210> 64
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 64

gaattcctta ag

12

<210> 65

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Peptide

<223> Xaa at position 2, 5 is a variable residue
 Xaa at position 8 is a threonine or a serine
 residue

<221> VARIANT

<222> (1)...(8)

<223> Xaa = Any Amino Acid

<400> 65

Gly Xaa Thr Gly Xaa Gly Lys Xaa
 1 5

<210> 66

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Peptide

<223> Xaa at position 2, 3, 4, 8 is a hydrophobic residue
 Xaa at position 11 is a variable residue

<221> VARIANT

<222> (1)...(12)

<223> Xaa = Any Amino Acid

<400> 66

Ser Xaa Xaa Xaa Phe Asp Glu Xaa Glu Lys Xaa His
 1 5 10

<210> 67

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 67

gtaggctggg

10

<210> 68

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 68
gcaaggatgg 10

<210> 69
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 69
gtaaggcag 10

<210> 70
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 70
gtgagtaggg 10

<210> 71
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 71
tctttcccag 10

<210> 72
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 72
tttaattcag 10

<210> 73
<211> 10
<212> DNA
<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 73

tgttttgcag

10

<210> 74

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 74

ttcttcccaag

10

<210> 75

<211> 11

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 75

cactgcagaa g

11

<210> 76

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 76

caatgctggaa

10

<210> 77

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of TORB

<400> 77

tggcttctgg

10

<210> 78

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of TORB

<400> 78
gcaagagaac 10

<210> 79
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 79
gtcagcggga 10

<210> 80
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 80
gtgagtcac 10

<210> 81
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 81
gttcttgcag 10

<210> 82
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 82
gttggtccag 10

<210> 83
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 83
gcaaactcag 10

<210> 84
<211> 9

<212> DNA
 <213> Unknown

<220>
 <223> Exon/intron of TORB

<400> 84
 tgttctgag

9

<210> 85
 <211> 11
 <212> DNA
 <213> Unknown

<220>
 <223> Exon/intron of TORB

<400> 85
 ctctcaagct g

11

<210> 86
 <211> 10
 <212> DNA
 <213> Unknown

<220>
 <223> Exon/intron of TORB

<400> 86
 caatgcaggg

10

<210> 87
 <211> 10
 <212> DNA
 <213> Unknown

<220>
 <223> Exon/intron of TORB

<400> 87
 tggcctgtgg

10

<210> 88
 <211> 378
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 1

<221> misc_feature
 <222> (1)...(378)
 <223> n = A,T,C or G

<400> 88
 ctggggaaaga caaaggccaat caggagtggg gaagaaaacac ggcaaaaatgt agccacattt 60
 acagccata aganagccag caaagccgtc tagcctccaa gcaccttgcg aaacctcaag 120
 tactgcggtc tggtaagctc ctggcccaga ggggacggcg gtccaggng ccctcccttt 180
 gctggtcctg cctattctaa agccctggcc cgnctccttc cggaaaagcc ccttggtgcc 240

actgccactg ccaccanttt gcnccccctac ccctgtnctg ctcctccac cccaaaggcag 300
atgcggnnng ngaaaggaaa cantttggtc ctcctggtc ggctcgngga agactcctca 360
ccatccttcc tgtcttcc 378

<210> 89
<211> 402
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 2

<400> 89
gaatatttac gagggtggtc tgaacagtga ctatgtccac ctgtttgtgg ccacattgct 60
ctttccacat gcttcaaaca tcaccttcta caaggcaagg atggaagttt ggaatccctt 120
cctggatgtc atcggggttg gggctcttt gttgtggat gagatttggg agttctatgt 180
tcaaataatgagt gagcccgaa aacgggtcat gtctcagttc cccttggaaa ggtgtagaag 240
ttaagagatggat gagatgcgtg gaggcgtttaa taccatcaaa gctttgtggt gggttctgaa 300
aattcggtcca gtgagatgtt agggctatgg gattttagag gtggacatga tcaaattccat 360
cttagagatc aacacatctc actcattttt attttcttat tt 402

<210> 90
<211> 200
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 3

<400> 90
ctcgactatt atgacactgggt ggatggggtc tcctaccaga aagccatgtt catatttctc 60
agtaagggtc agggcttagga catgtatggat gggccccgag cccaaaggctc tgagctccag 120
gagaaaaaccct tgcccttacc cactgggatt gtttgcagc aatgctggag cagaaaggat 180
cacagatgtg gctttggatt 200